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L R Y T P H P A Y A T F C R P K E N W W 63  
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Q Y T Q G R R Y A S T P Q K F Y L T P P 83  
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D G H A G C A C S Q A V S E R L F Y Y I 163  
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A V S L L P H E T L L E I E N A V E S G 183  
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T G E S T D I D V K E A L I N A F K R L 243  
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D N D I S L E A Q V G D P N S F L N Y L 263  
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V L R V A F S G A T A C V A H V D G V D 283  
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L H V A N T G D S R A M L G V Q E E D G 303  
 CTT CAT GTG GCC AAT ACT GGC GAT AGC AGA GCC ATG CTG GGT GTG CAG GAA GAG GAC GGC 909

S W S A V T L S N D H N A Q N E R E L E 323  
 TCA TGG TCA GCA GTC ACG CTG TCT AAT GAC CAC AAT GCT CAA AAT GAA AGA GAA CTA GAA 969

R L K L E H P K S E A K S V V K Q D R L 343  
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L G L L M P F R A F G D V K F K W S I D 363  
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F I P P N Y H T P P Y L T A E P E V T Y 403  
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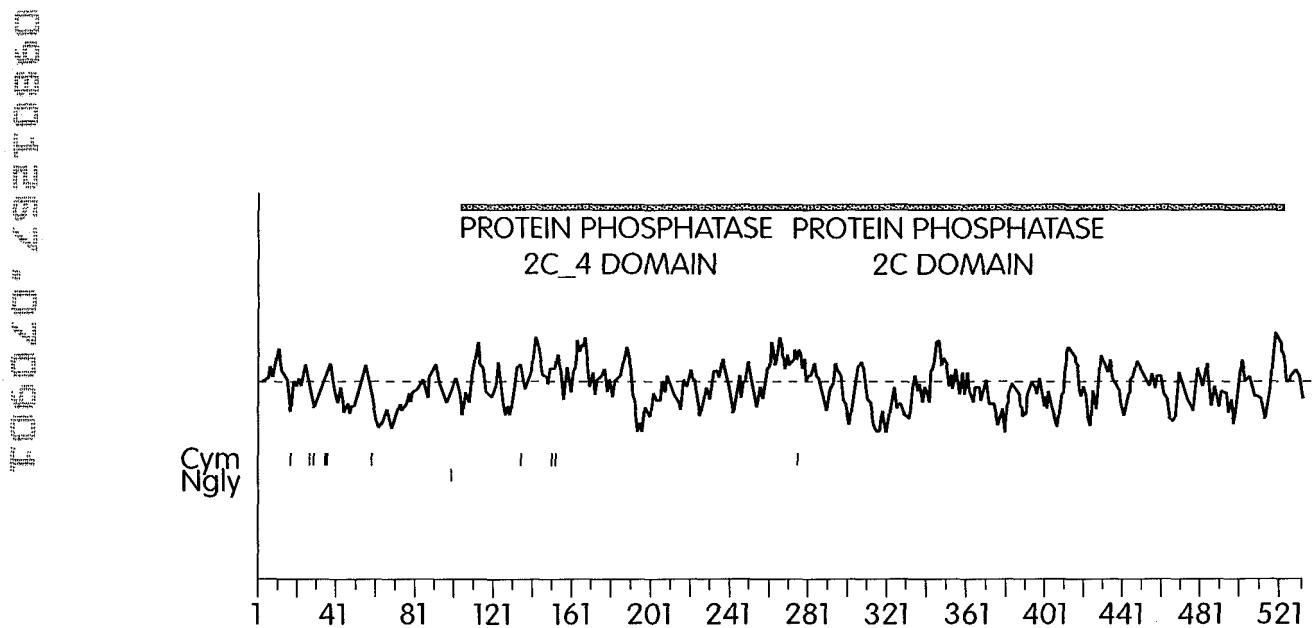


Fig. 2

PP2C: domain 1 of 1, from 173 to 461: score 261.3, E = 1.3e-74

\*->ldvgvsrmqgwrksmeDahialknlnsssgkdswsffavfDGhgGs SEQ ID NO:4  
 1 +++++ + r +++ +++++++ ++ s++ s+ +f +++ +  
 26583 173 LLEIENAVESGRALLPILQWHKHPNDYF-SKEASKLYFNSLRTYWQE 218 SEQ ID NO:2  
  
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 26583 219 LIDLNTGESTDIDVKEALINAFKRLDN-----DISLEAQVGDPNSFLNY 262  
  
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 26583 263 LVLR-----VAFSGATAACVAHVDGVDLHVANTGDSRAMLGQ 299  
  
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 26583 350 FRAFGDVKFKWSIDLQKRVIEsgPdQ1NDnEYTKFIPPnyhtpPYLTAEQ 399  
  
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 +vt + + +l+p+ D+F+L+A+DGLW+ + + + q+vv iv + l+ + +  
 26583 400 EVT-YHRLRPQ-DKFLVLATDGLWETMHRQDVVRIVGEYLTGM-----H 441  
  
 meaaeklvdeaiargaeDni<-\*  
 ++ ++ + + g ++  
 26583 442 HQQPIAVGGYKVTLGQMHGL 461

Fig. 3A

PP2C\_4: domain 1 of 1, from 99 to 523: score 338.5, E = 7.6e-98

\*->es.sgknlglyglgessmgwrkpmEDahvirp.....ffgvfD SEQ ID NO:5

+ gkn +++ g+ +s++ +++ p+ED+ ++ + +++++ + gVfd

26583 99 PEFDGKVNSSLGF-DSNQLPANAPIEDRRSAATclqtrgmLLGVFD 144 SEQ ID NO:2

GHGGseaakflsknlheilaeelsfdkdeslkene.e.lk.d.ep....

GH+G +++ +s++l+ ++a +l +++ ++ en+ e+++ + ++ + ++

26583 145 GHAGCACSQAVSERLFYYIAVSLLPHETLLEIENAvEsGRaLLPIlqwnk 194

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++++ +++ ++ ++ ++++++e +ln+g++++ dv+eal++aF+r+d

26583 195 hpndyfskeasklyfnslrTYWqElIdLNtGESTDIDVKEALINAFKRLD 244

eei.....sTAvalirgnklyvANvGDSRa

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26583 245 NDISleaqvgdponsflnylvrvafsgATACVAHVDGVDLHVANTGDSRA 294

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+L+ + +d+sw sav L++DH++ ne+E+eR++ +++++ e +++

26583 295 MLGVQEEDgSW-----SAVTL SNDHNAQNEREELERLKLEHPKSE--AKS 336

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26583 337 VVKQD----RLLGL---LMPFRAFGDVFKWsIDLqKrVIEsgpdqLNd 378

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v

26583 523 V 523

Fig. 3B

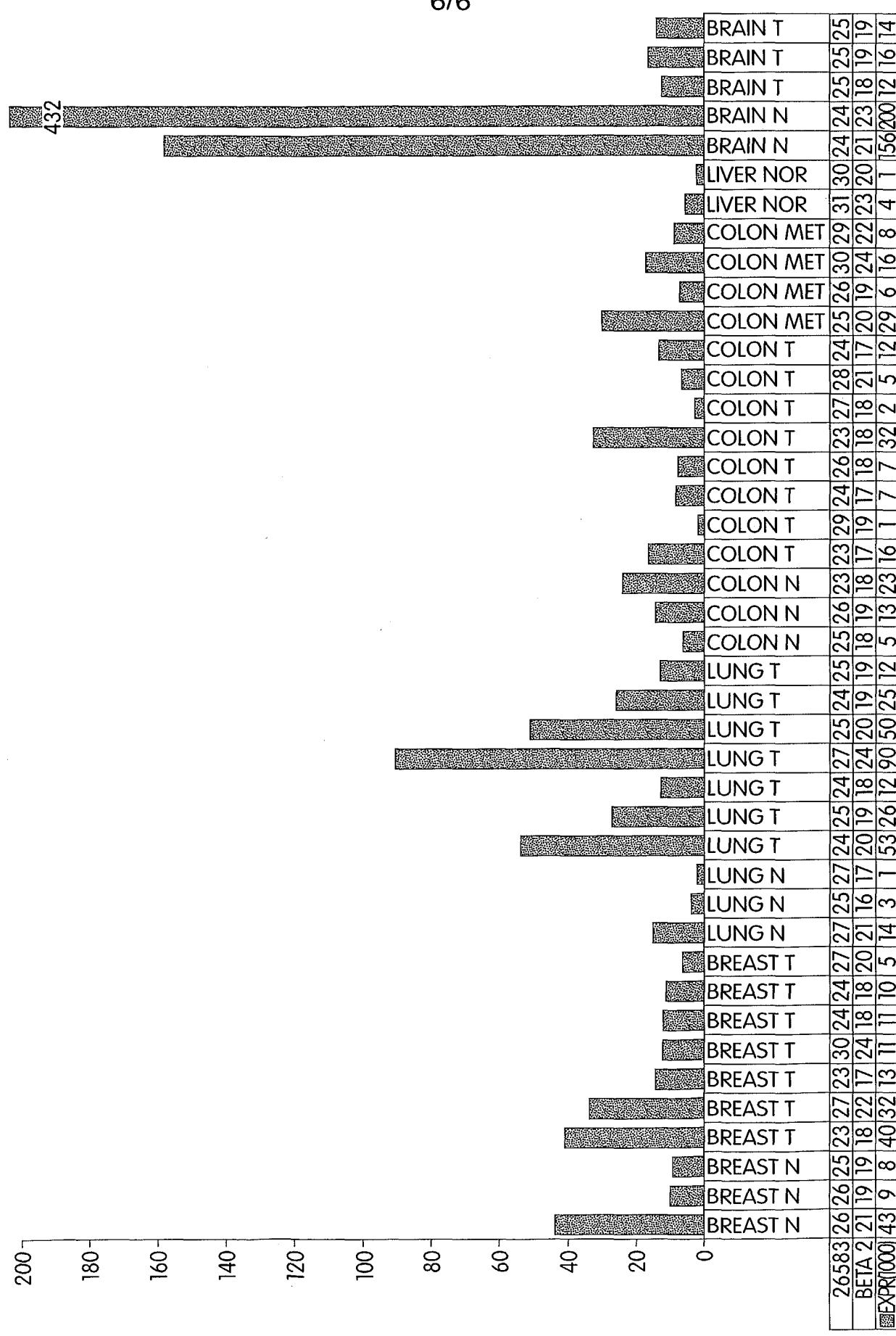


Fig. 4